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Comparison between Livestock and Community associated MRSA in Europe



Cavaco, LM¹; Miragaia, M²; Rolo, J²; Conceição T²; Hasman, H.¹; Aarestrup, FM¹; de Lencastre, H.^{2,3}

1- Research Group for Microbial Genomics and Antimicrobial Resistance; National Food Institute, Technical University of Denmark; Kgs Lyngby, Denmark; 2- Laboratory of Molecular Genetics, Instituto de Tecnologia Química e Biológica (ITQB), Universidade Nova de Lisboa, Oeiras, Portugal; 3- Laboratory of Microbiology, The Rockefeller University, USA

Background

Community associated (CA)-MRSA has been in the latest years a major issue in Public Health, showing increasing prevalence worldwide, including Europe and representing a challenge to infection control. Meanwhile, Livestock associated (LA)-MRSA emerged and have been found widespread among livestock populations being considered an emerging threat to Public Health, due to occupational transmission to humans.

As part of the European Project CONCORD, which focused on the study of CA and LA-MRSA populations in Europe, we have collected strains from human and animal origin in different countries in order to shed light on the origin and evolution of CA and LA-MRSA.

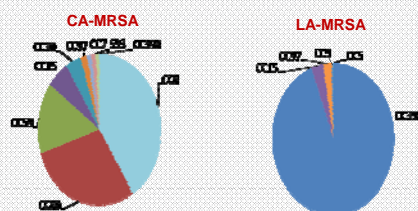
Methods

A total of 180 CA-MRSA isolates from humans in 16 countries and 649 LA-MRSA (486 from pigs and 163 from cattle) from nine countries in Europe were collected.

Species identification was confirmed by PCR and/or biochemical reactions. Isolates were typed by *spa* typing and MLST. Clonal complexes (CC) were defined based on the Ridom *spa* server data and/or confirmatory MLST using the e-BURST algorithm. PVL was tested for all human isolates. All human isolates and a sample of 27 LA-MRSA isolates were tested for antimicrobial susceptibility.

SCCmec typing was performed in all CA-MRSA and in 135 selected LA-MRSA. Additional subtyping was performed for type IV elements. In addition, the nucleotide sequence of an internal fragment of *ccrC* was determined in a subset of isolates from both populations harboring SCCmec type V.

Figure 1 – Clonal lineages present in CA-MRSA and LA-MRSA



Results

The most prevalent genetic lineages among CA-MRSA were CC8 (40%), followed by CC80 (28%) and CC59 (15%). Among the LA-MRSA 94% of the isolates belonged to CC398, while only 6% belonged to other Clonal complexes (1, 5, 9 and 97). CC398, CC97 and CC1 were identified in both CA and LA-MRSA, but in different proportions (Figure 1). In addition, we found that, some MRSA isolates collected from humans and animals belonged to the same clones (ST398-VII; ST5-IVa), but harbored different *spa* types. The distribution of SCCmec showed a higher variability in CA-MRSA with high prevalence of type IV. Among LA-MRSA SCCmec was differently distributed with predominance of type Vc (5C2&5) in pigs and IV among veal calves (Figure 2).

We found that, the overall antimicrobial resistance was higher among isolates collected from animals than among isolates collected from humans with the exception of penicillin and erythromycin (Figure 4). Sequencing of *ccrC* alleles demonstrated similarities between SCCmec elements in LA and CA-MRSA and methicillin-resistant coagulase-negative staphylococci (MRCoNS) from humans (Figure 5).

Figure 2– Distribution of SCCmec types in CA-MRSA and LA-MRSA.

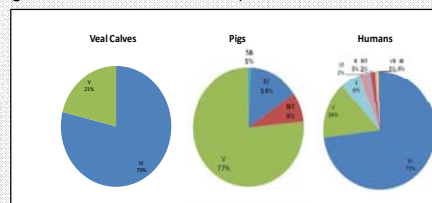
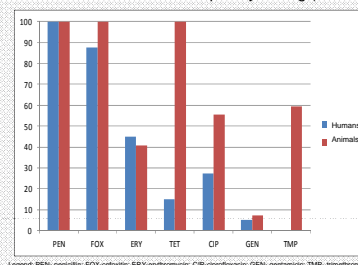


Figure 3 – Results of antimicrobial susceptibility testing (% resistant isolates).



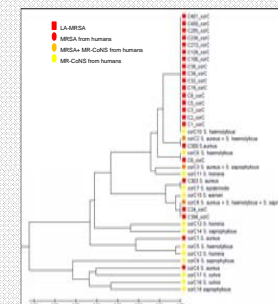
Legend: PEN: penicillin; FOX: cefoxitin; ERY: erythromycin; CIP: ciprofloxacin; GEN: gentamicin; TMP: trimethoprim

Discussion and conclusions

The molecular characterization of MRSA isolates from the community and livestock, have shown that different clonal types prevail among each of these settings. Only a small proportion of genotypes (6.27%, 14/223) were common to animals and humans, suggesting that the extent of dissemination between the two settings is not frequent. Also our results suggest that dissemination probably occurs in the two directions: from animals to humans and from humans to animals. Additionally, we observed that SCCmec is more diverse among humans than animals and that different animal species could be reservoirs for different SCCmec types: pigs for SCCmec V and calves for SCCmec IV.

Moreover, the results indicate that CoNS may be acting as donors of SCCmec to LA-MRSA.

Figure 4– Linearized unrooted UPGMA tree of *ccrC* internal region from FA-MRSA and *ccrC* of *S. aureus* and coagulase- negative staphylococci



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